



SEQUENCE LISTING

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STROMINGER, Jack L

<120> MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING
DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES
THEREFOR

<130> HAR-005

<140> 09/248,964

<141> 1999-02-12

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<151> 1997-08-15

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<151> 1998-02-19

<150> 60/024,077

<151> 1996-08-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Fos fusion

<220>

<221> CDS

<222> (1)..(735)

<220>

<221> misc_feature

<222> (1)..(21)

<223> 3' end of secretory signal

<220>

<221> misc_structure

<222> (22)..(594)

<223> DRA*0101 extracellular domain

<220>

<221> misc_feature

<222> (595)..(615)

<223> Linker sequence

<220>

<221> misc_feature

<222> (616)..(735)

<223> Fos leucine zipper domain

<400> 1

gta tct ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag 48

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TECH CENTER 1600/2900

Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
 1 5 10 15

gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac 96
 Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
 20 25 30

ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg
 144
 Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
 35 40 45

gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa
 192
 Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
 50 55 60

ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg
 240
 Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
 65 70 75 80

aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta
 288
 Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
 85 90 95

act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc
 336
 Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
 100 105 110

atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg
 384
 Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
 115 120 125

ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc
 432
 Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
 130 135 140

ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc
 480
 Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
 145 150 155 160

ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc
 528
 Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
 165 170 175

ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct
 576
 Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
 180 185 190

ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat
 624

Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp
195 200 205

aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg
672

Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
210 215 220

cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc
720

Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
225 230 235 240

atc ctg gcc gcc cat tgagaattct atgac
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Ile Leu Ala Ala His
245

<210> 2

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Fos fusion

<220>

<221> misc_feature

<222> (1)..(7)

<223> 3' end of secretory signal

<220>

<221> misc_structure

<222> (8)..(198)

<223> DRA*0101 extracellular domain

<220>

<221> misc_feature

<222> (199)..(205)

<223> Linker sequence

<220>

<221> misc_feature

<222> (206)..(245)

<223> Fos leucine zipper domain

<400> 2

Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
1 5 10 15

Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
20 25 30

Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
35 40 45

Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
50 55 60

Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu	Ile	Met	65	70	75	80
Thr	Lys	Arg	Ser	Asn	Tyr	Thr	Pro	Ile	Thr	Asn	Val	Pro	Pro	Glu	Val	85	90	95	
Thr	Val	Leu	Thr	Asn	Ser	Pro	Val	Glu	Leu	Arg	Glu	Pro	Asn	Val	Leu	100	105	110	
Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val	Thr	Trp	115	120	125	
Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr	Val	Phe	130	135	140	
Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu	Pro	Phe	145	150	155	160
Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His	Trp	Gly	165	170	175	
Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro	Ser	Pro	180	185	190	
Leu	Pro	Glu	Thr	Thr	Glu	Val	Asp	Gly	Gly	Gly	Gly	Gly	Leu	Thr	Asp	195	200	205	
Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser	Ala	Leu	210	215	220	
Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu	Glu	Phe	225	230	235	240
Ile	Leu	Ala	Ala	His												245			

<210> 3

<211> 771

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Jun fusion

<220>

<221> CDS

<222> (1)..(756)

<220>

<221> misc_feature

<222> (1)..(21)

<223> 3' end of secretory signal

<220>

<221> misc_feature

<222> (22)..(615)

<223> DRB1*1501 extracellular domain

<220>

<221> misc_feature
 <222> (616)..(636)
 <223> Linker sequence

<220>
 <221> misc_feature
 <222> (637)..(756)
 <223> Jun leucine zipper domain

<400> 3
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 1 5 10 15
 cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg 96
 Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
 20 25 30
 ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac
 144
 Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
 35 40 45
 agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac
 192
 Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
 50 55 60
 gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cgg gcc
 240
 Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
 65 70 75 80
 gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc
 288
 Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
 85 90 95
 aca gtg cag cgg cga gtc caa cct aag gtg act gta tat cct tca aag
 336
 Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
 100 105 110
 acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt
 384
 Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
 115 120 125
 ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa
 432
 Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
 130 135 140
 gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg
 480
 Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
 145 150 155 160

acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag
 528
 Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
 165 170 175

gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca
 576
 Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
 180 185 190

gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga
 624
 Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
 195 200 205

ggt ggc ggc ggt cgc atc gcc cgg ctc gag gaa aaa gtg aaa acc ttg
 672
 Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
 210 215 220

aaa gct cag aac tcg gag ctc gcg tcc acg gcc aac atg ctc agg gaa
 720
 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
 225 230 235 240

cag gtg gca cag ctt aaa cag aaa gtc atg aac cat tgagaattct atgac
 771
 Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
 245 250

<210> 4
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DR2-Jun fusion

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 <222> (1)..(7)
 <223> 3' end of secretory signal

<220>
 <221> misc_feature
 <222> (8)..(205)
 <223> DRB1*1501 extracellular domain

<220>
 <221> misc_feature
 <222> (206)..(212)
 <223> Linker sequence

<220>
 <221> misc_feature
 <222> (213)..(252)
 <223> Jun leucine zipper domain

<400> 4

Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp
1 5 10 15

Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
20 25 30

Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
35 40 45

Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
50 55 60

Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
65 70 75 80

Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
85 90 95

Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
100 105 110

Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
115 120 125

Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
130 135 140

Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
145 150 155 160

Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
165 170 175

Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
180 185 190

Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
195 200 205

Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
210 215 220

Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
225 230 235 240

Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
245 250

<210> 5

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 5
gtatctctcg agaaaagaga gatcaaagaa gaacatgtga tc 42

<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 6
gtcatagaat tctcaatggg cggccaggat gaactccag 39

<210> 7
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 7
gtatctctcg agaaaagaga gggggacacc cgaccacgtt tc 42

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 8
gtcatagaat tctcaatggg tcatgacttt ctgtttaag 39

<210> 9
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic,
biotin ligase recognition sequence

<400> 9
Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp
1 5 10

<210> 10
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic,
linker sequence

<400> 10
Ser Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 11
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-IgG fusion

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<222> (1)..(1437)

<220>
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<222> (1)..(15)
<223> 3' end of secretory signal

<220>
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<222> (16)..(588)
<223> DRA*0101 extracellular domain

<220>
<221> misc_feature
<222> (589)..(609)
<223> Linker

<220>
<221> misc_feature
<222> (610)..(729)
<223> Fos leucine zipper domain

<220>
<221> misc_feature
<222> (730)..(1437)
<223> IgG domain

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1 5 10 15

ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac ttt gat 96
Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
20 25 30

ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg
 144
 Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
 35 40 45

cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca
 192
 Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
 50 55 60

ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg aca aag
 240
 Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
 65 70 75 80

cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg
 288
 Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
 85 90 95

ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc atc tgt
 336
 Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
 100 105 110

ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg ctt cga
 384
 Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
 115 120 125

aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc ctg ccc
 432
 Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
 130 135 140

agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc ctg ccc
 480
 Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
 145 150 155 160

tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc ttg gat
 528
 Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp
 165 170 175

gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct ctc cca
 576
 Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro
 180 185 190

gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat aca ctc
 624
 Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp Thr Leu
 195 200 205

caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg cag acc
 672
 Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr

210	215	220
gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc atc ctg		
720		
Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu		
225	230	235 240
gcc gcc cat gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt		
768		
Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys		
	245	250 255
cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc		
816		
Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val		
	260	265 270
ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc		
864		
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser		
	275	280 285
ccc ata gtc aca tgt gtg gtg gtg gat gtg agc gag gat gac cca gat		
912		
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp		
	290	295 300
gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag		
960		
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln		
305	310	315 320
aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt		
1008		
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser		
	325	330 335
gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa		
1056		
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys		
	340	345 350
tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc		
1104		
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile		
	355	360 365
tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct		
1152		
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro		
	370	375 380
cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg		
1200		
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met		
	385	390 395 400

gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac
1248

Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
405 410 415

ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct
1296

Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
420 425 430

gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac
1344

Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
435 440 445

tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg
1392

Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
450 455 460

cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aaa
1437

His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
465 470 475

tgagaattc
1446

<210> 12

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-IgG fusion

<220>

<221> misc_feature

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<223> 3' end of secretory signal

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<221> misc_feature

<222> (6)..(196)

<223> DRA*0101 extracellular domain

<220>

<221> misc_feature

<222> (197)..(203)

<223> Linker

<220>

<221> misc_feature

<222> (204)..(243)

<223> Fos leucine zipper domain

<220>

<221> misc_feature

<222> (244)..(479)

<223> IgG domain

<400> 12

Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu
1 5 10 15

Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
20 25 30

Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45

Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60

Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80

Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
85 90 95

Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
100 105 110

Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
115 120 125

Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
130 135 140

Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145 150 155 160

Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp
165 170 175

Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro
180 185 190

Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Glu Thr Asp Thr Leu
195 200 205

Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr
210 215 220

Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu
225 230 235 240

Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
245 250 255

Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser

275	280	285
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp		
290	295	300
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln		
305	310	315
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser		
	325	330
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys		
	340	345
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile		
	355	360
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro		
	370	375
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met		
385	390	395
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn		
	405	410
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser		
	420	425
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn		
	435	440
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu		
	450	455
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys		
465	470	475

<210> 13

<211> 1851

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-IgM fusion

<220>

<221> CDS

<222> (1)..(1836)

<220>

<221> misc_feature

<222> (1)..(75)

<223> 3' end of secretory signal

<220>

<221> misc_feature

<222> (76)..(648)

<223> DRA*0101 extracellular domain

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<221> misc_feature

<222> (649)..(669)

<223> Linker

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<222> (670)..(789)

<223> Fos leucine zipper domain

<220>

<221> misc_feature

<222> (790)..(1836)

<223> IgG domain

<400> 13

atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg	48
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val	
1 5 10 15	

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc	96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile	
20 25 30	

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg	
144	
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met	
35 40 45	

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag	
192	
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys	
50 55 60	

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag	
240	
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu	
65 70 75 80	

gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa	
288	
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu	
85 90 95	

atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca	
336	
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro	
100 105 110	

gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac	
384	
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn	
115 120 125	

gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc	
432	

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
130 135 140
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca
480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145 150 155 160
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc
528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
165 170 175
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac
576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
180 185 190
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca
624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195 200 205
agc cct ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta
672
Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu
210 215 220
act gat aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct
720
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
225 230 235 240
gcg ttg cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg
768
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
245 250 255
gag ttc atc ctg gcc gcc cac gtc gca gaa atg aac ccc aat gta aat
816
Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn
260 265 270
gtg ttc gtc cca cca cgg gat ggc ttc tct ggc cct gca cca cgc aag
864
Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys
275 280 285
tct aaa ctc atc tgc gag gcc acg aac ttc act cca aaa ccg atc aca
912
Ser Lys Leu Ile Cys Glu Ala Thr Asn Phe Thr Pro Lys Pro Ile Thr
290 295 300
gta tcc tgg cta aag gat ggg aag ctc gtg gaa tct ggc ttc acc aca
960
Val Ser Trp Leu Lys Asp Gly Lys Leu Val Glu Ser Gly Phe Thr Thr
305 310 315 320

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 1008
 Asp Pro Val Thr Ile Glu Asn Lys Gly Ser Thr Pro Gln Thr Tyr Lys
 325 330 335

gtc ata agc aca ctt acc atc tct gaa atc gac tgg ctg aac ctg aat
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 Val Ile Ser Thr Leu Thr Ile Ser Glu Ile Asp Trp Leu Asn Leu Asn
 340 345 350

gtg tac acc tgc cgt gtg gat cac agg ggt ctc acc ttc ttg aag aac
 1104
 Val Tyr Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Leu Lys Asn
 355 360 365

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 1152
 Val Ser Ser Thr Cys Ala Ala Ser Pro Ser Thr Asp Ile Leu Asn Phe
 370 375 380

act att cct cct tcc ttt gcc gac atc ttc ctt agc aag tcc gct aac
 1200
 Thr Ile Pro Pro Ser Phe Ala Asp Ile Phe Leu Ser Lys Ser Ala Asn
 385 390 395 400

ctg acc tgt ctg gtc tca aac ctg gca acc tat gaa acc ctg agt atc
 1248
 Leu Thr Cys Leu Val Ser Asn Leu Ala Thr Tyr Glu Thr Leu Ser Ile
 405 410 415

tcc tgg gct tct caa agt ggt gaa cca ctg gaa acc aaa att aaa atc
 1296
 Ser Trp Ala Ser Gln Ser Gly Glu Pro Leu Glu Thr Lys Ile Lys Ile
 420 425 430

atg gaa agc cat ccc aat ggc acc ttc agt gct aag ggt gtg gct agt
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 Met Glu Ser His Pro Asn Gly Thr Phe Ser Ala Lys Gly Val Ala Ser
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gtt tgt gtg gaa gac tgg aat aac agg aag gaa ttt gtg tgt act gtg
 1392
 Val Cys Val Glu Asp Trp Asn Asn Arg Lys Glu Phe Val Cys Thr Val
 450 455 460

act cac agg gat ctg cct tca cca cag aag aaa ttc atc tca aaa ccc
 1440
 Thr His Arg Asp Leu Pro Ser Pro Gln Lys Lys Phe Ile Ser Lys Pro
 465 470 475 480

aat gag gtg cac aaa cat cca cct gct gtg tac ctg ctg cca cca gct
 1488
 Asn Glu Val His Lys His Pro Pro Ala Val Tyr Leu Leu Pro Pro Ala
 485 490 495

cgt gaa caa ctg aac ctg agg gag tca gcc aca gtc acc tgc ctg gtg
 1536
 Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Val Thr Cys Leu Val
 500 505 510

aag ggc ttc tct cct gca gac atc tct gtg caa tgg aag cag agg ggc
1584

Lys Gly Phe Ser Pro Ala Asp Ile Ser Val Gln Trp Lys Gln Arg Gly

515 520 525
cag ctc tta ccc cag gag aag tat gtg acc agt gcc ccg atg cca gag
1632

Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu
530 535 540

cct ggg gcc cca ggc ttc tac ttt acc cac agc atc ctg act gtg aca
1680

Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr
545 550 555 560

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1728

Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His
565 570 575

gag gcc ctg cca cac ctg gtg acc gag agg acc gtg gac aag tcc act
1776

Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr
580 585 590

ggt aaa ccc aca ctg tac aat gtc tcc ctg atc atg tct gac aca ggc
1824

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

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Gly Thr Cys Tyr
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<220>

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<223> DRA*0101 extracellular domain

<220>

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<223> Linker

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 <223> IgG domain

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			20					25					30		
Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	Ser	Gly	Glu	Phe	Met
		35					40					45			
Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	His	Val	Asp	Met	Ala	Lys	Lys
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Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	Gly	Arg	Phe	Ala	Ser	Phe	Glu
65					70				75						80
Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu
				85					90					95	
Ile	Met	Thr	Lys	Arg	Ser	Asn	Tyr	Thr	Pro	Ile	Thr	Asn	Val	Pro	Pro
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Glu	Val	Thr	Val	Leu	Thr	Asn	Ser	Pro	Val	Glu	Leu	Arg	Glu	Pro	Asn
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Val	Leu	Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val
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Thr	Trp	Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr
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Val	Phe	Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu
				165					170					175	
Pro	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His
			180					185					190		
Trp	Gly	Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro
	195						200					205			
Ser	Pro	Leu	Pro	Glu	Thr	Thr	Glu	Val	Asp	Gly	Gly	Gly	Gly	Gly	Leu
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Thr	Asp	Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	Ser
225					230					235					240
Ala	Leu	Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	Leu

245										250					255									
Glu	Phe	Ile	Leu	Ala	Ala	His	Val	Ala	Glu	Met	Asn	Pro	Asn	Val	Asn									
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Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Ser	Gly	Pro	Ala	Pro	Arg	Lys									
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Ser	Lys	Leu	Ile	Cys	Glu	Ala	Thr	Asn	Phe	Thr	Pro	Lys	Pro	Ile	Thr									
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Asp	Pro	Val	Thr	Ile	Glu	Asn	Lys	Gly	Ser	Thr	Pro	Gln	Thr	Tyr	Lys									
325										330					335									
Val	Ile	Ser	Thr	Leu	Thr	Ile	Ser	Glu	Ile	Asp	Trp	Leu	Asn	Leu	Asn									
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370										375					380									
Thr	Ile	Pro	Pro	Ser	Phe	Ala	Asp	Ile	Phe	Leu	Ser	Lys	Ser	Ala	Asn									
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Leu	Thr	Cys	Leu	Val	Ser	Asn	Leu	Ala	Thr	Tyr	Glu	Thr	Leu	Ser	Ile									
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Ser	Trp	Ala	Ser	Gln	Ser	Gly	Glu	Pro	Leu	Glu	Thr	Lys	Ile	Lys	Ile									
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Val	Cys	Val	Glu	Asp	Trp	Asn	Asn	Arg	Lys	Glu	Phe	Val	Cys	Thr	Val									
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Thr	His	Arg	Asp	Leu	Pro	Ser	Pro	Gln	Lys	Lys	Phe	Ile	Ser	Lys	Pro									
465										470					475					480				
Asn	Glu	Val	His	Lys	His	Pro	Pro	Ala	Val	Tyr	Leu	Leu	Pro	Pro	Ala									
485										490					495									
Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Val	Thr	Cys	Leu	Val									
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Lys	Gly	Phe	Ser	Pro	Ala	Asp	Ile	Ser	Val	Gln	Trp	Lys	Gln	Arg	Gly									
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Gln	Leu	Leu	Pro	Gln	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met	Pro	Glu									
530										535					540									
Pro	Gly	Ala	Pro	Gly	Phe	Tyr	Phe	Thr	His	Ser	Ile	Leu	Thr	Val	Thr									
545										550					555					560				

Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His
565 570 575

Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr
580 585 590

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

Gly Thr Cys Tyr
610